

Figure 1

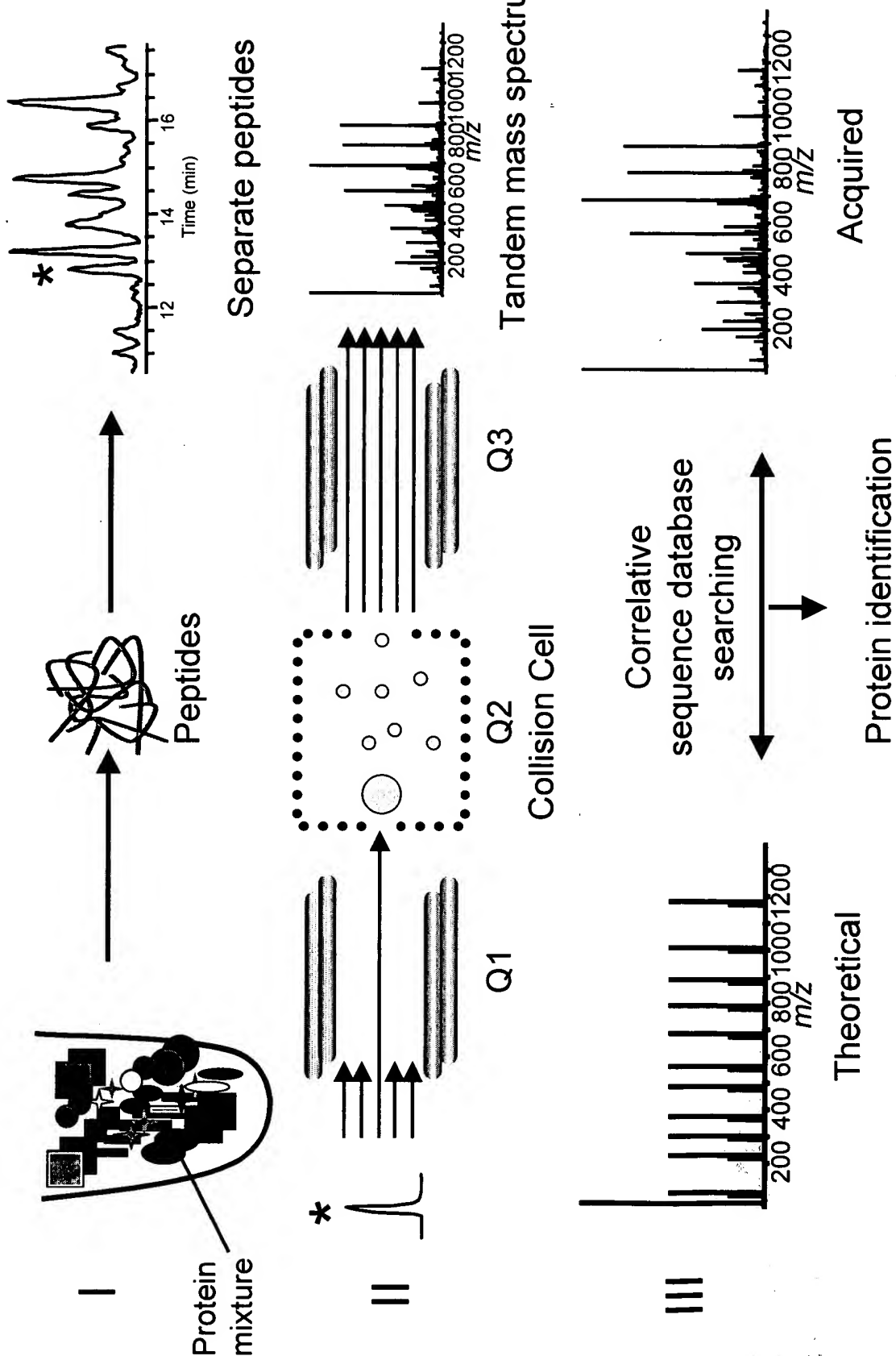
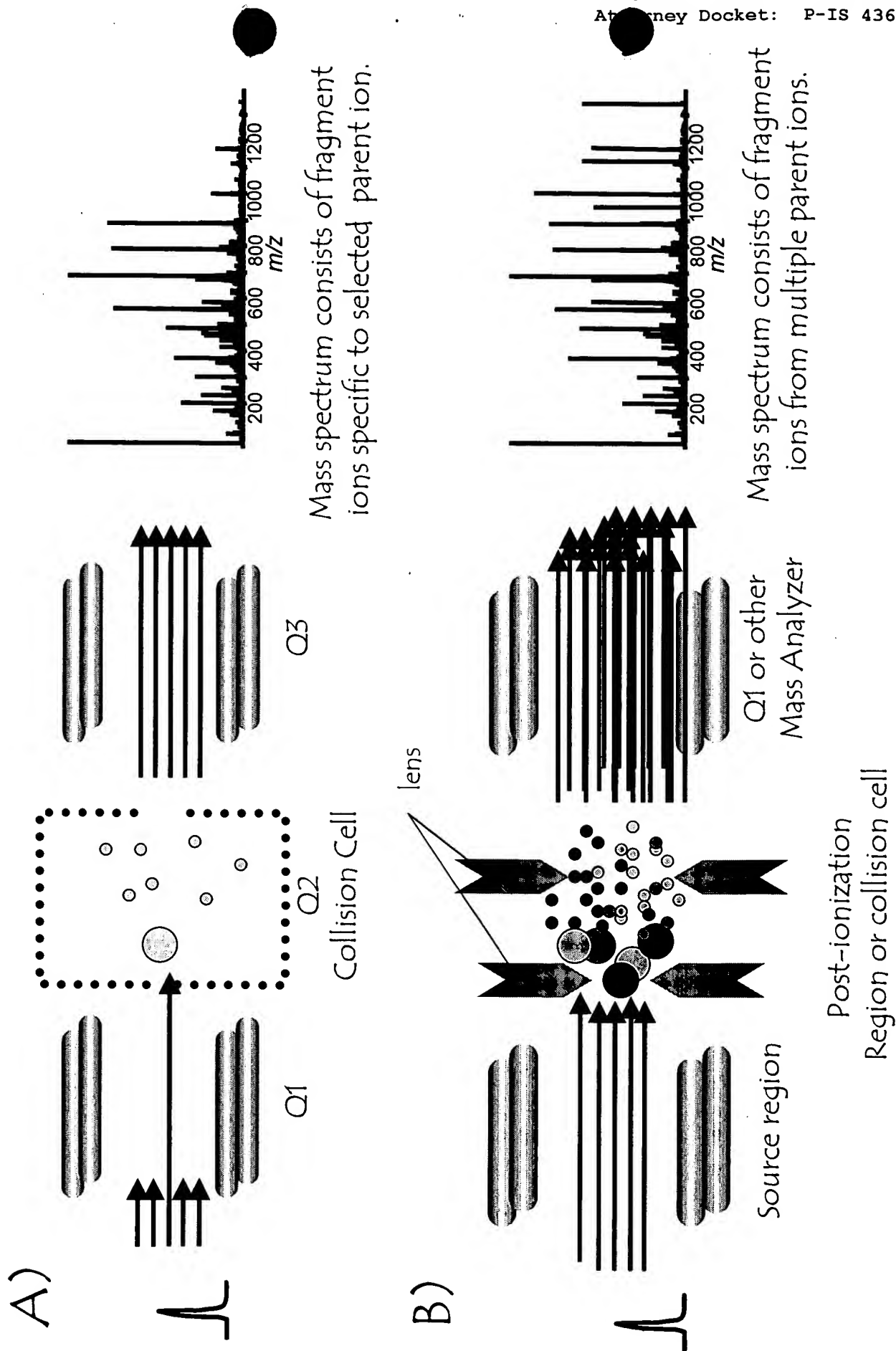


Figure 2



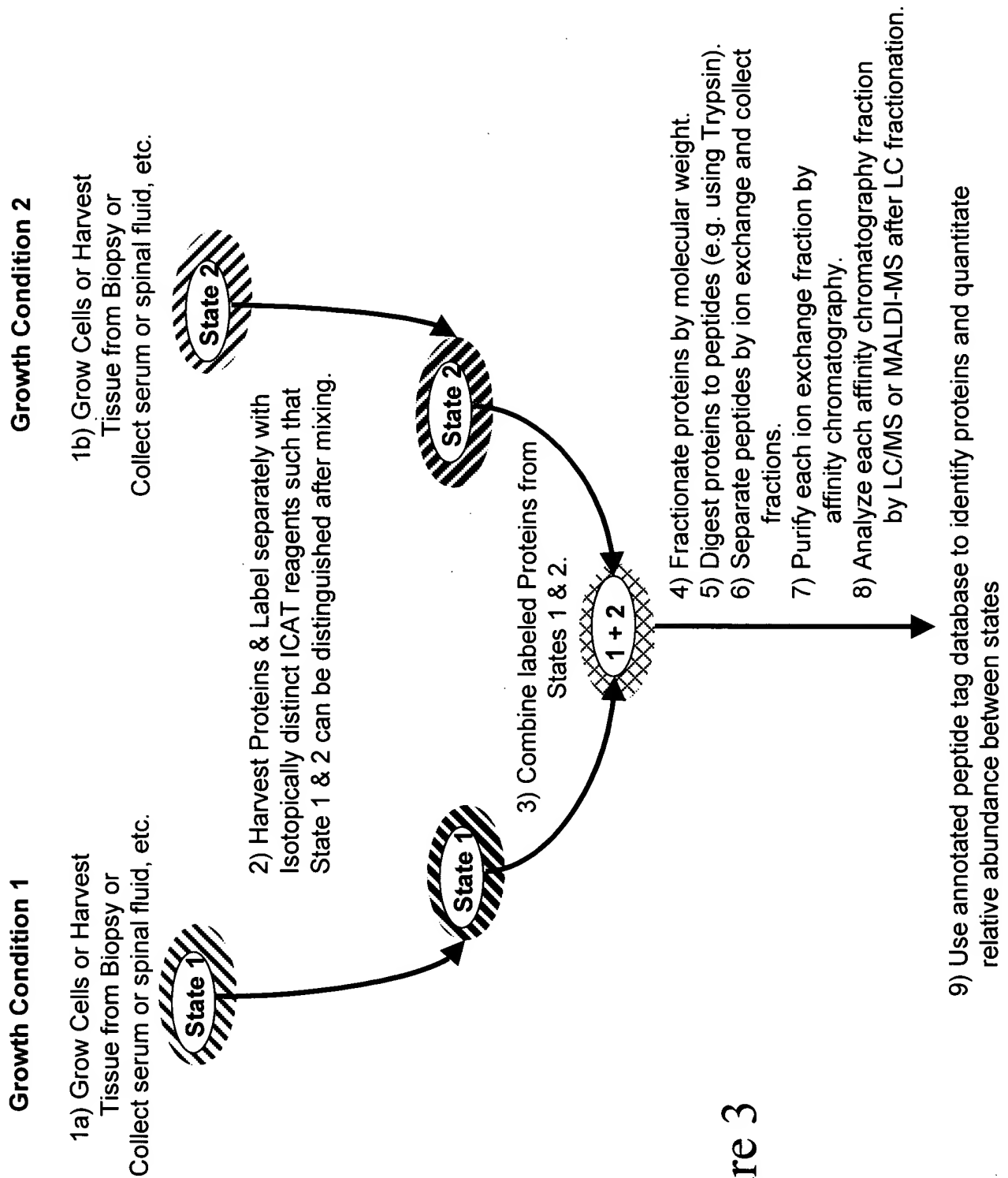
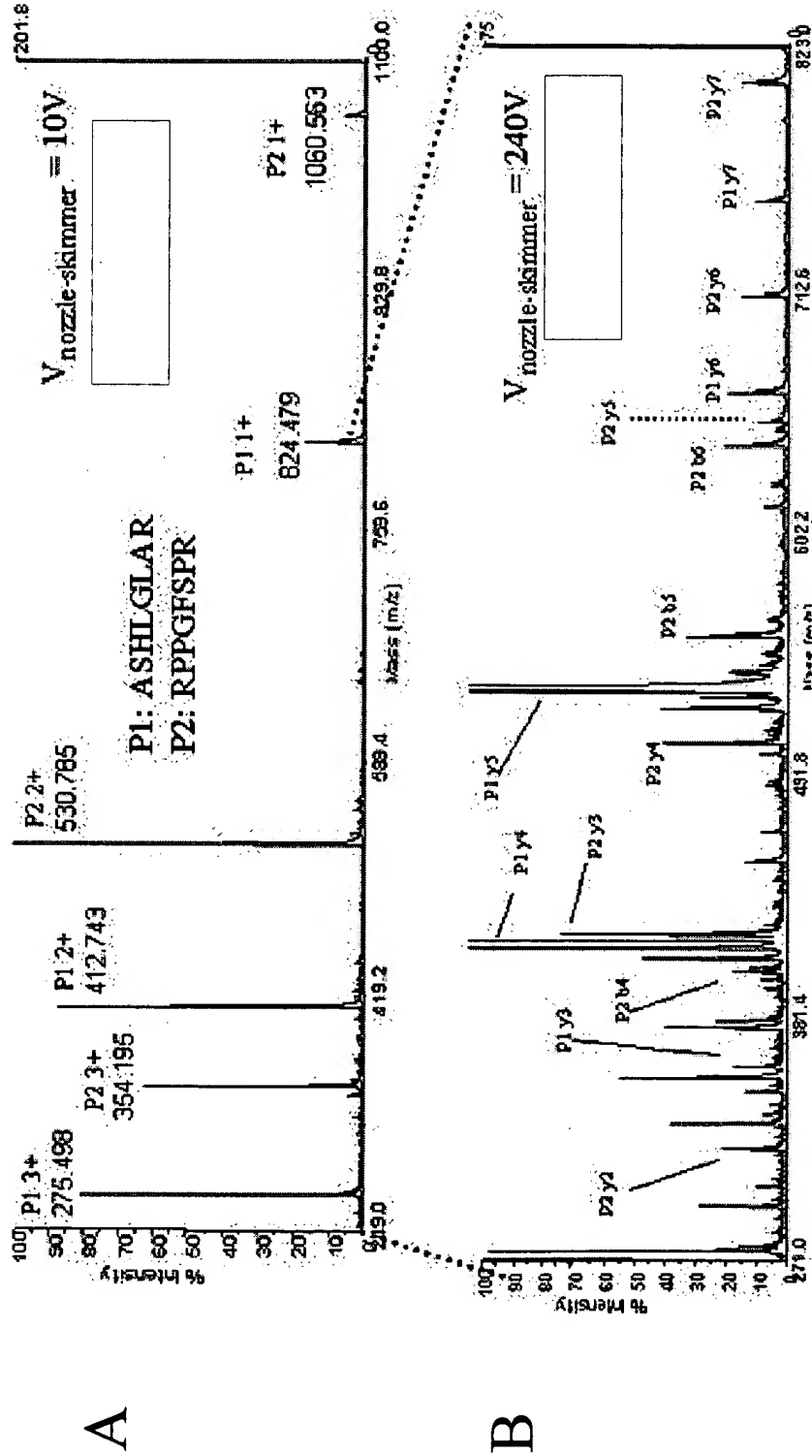


Figure 3

Figure 4



Human protein database:
60,884 sequence entries

C

Fragment ion masses used for analysis:

710.385
753.435
807.374
886.402
904.451
1001.564

Bradykinin RPPGFSPFR MH+ 1060.5676

at 10 PPM, 144 tryptic peptides match

13 matches using fragment ion constraint:

ACISEILPSK
GVRYSFGFK
RANLISQCR
RCGLPSSGKR
RDITLEASR
RERETLEK
RLTEEERK
RLVEVDSSR
RNLLDHHR
RPHAAQPGAR
RPPGFSPFR **
RPQTATASTK
RRPSAYQAL

ASHLGLAR MH+ 824.4739

at 10PPM, 57 tryptic peptides match

12 matches using fragment ion constraint:

ACYIKVK
ADPLPRR
AFVAFAAK
AFVFGRK
AHAEIRK
AHEAKIR
ALEAHKR
ALQFFAK
AMAIYKK
APDPRLR
ASHLGLAR **
AVAGHLTR

Figure 4